

condition or stage thereof in a eukaryotic organism comprising the steps of:

- (a) isolating mRNA from cells of one or more eukaryotic organisms which are known to have said disease or condition or a stage thereof (diseased sample), wherein said cells are obtained from, and originate from, a part of said organism distant to the area of said disease, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) isolating mRNA from corresponding cells of one or more corresponding normal eukaryotic organisms (normal sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (c) separating, by a non-sequence based separation technique, mRNA species or cDNA species present within each of the resulting isolated mRNA or isolated cDNA of step (a) and step (b), wherein the resulting separated mRNA species are optionally subjected to reverse transcription to obtain separated cDNA species;
- (d) selecting two or more mRNA species or two or more cDNA species from the resulting separated mRNA species or resulting separated cDNA species obtained in step (c), respectively, which are present at a different level in the normal sample than in

the diseased sample by identifying a signal corresponding to each mRNA species or cDNA species, wherein the resulting selected two or more mRNA species are optionally subjected to reverse transcription to obtain two or more selected cDNA species; and

- (e) isolating the resulting two or more selected mRNA species or resulting two or more selected cDNA species obtained in step (d) to obtain isolated selected mRNA species or isolated selected cDNA species, wherein the resulting isolated selected mRNA species are optionally subjected to reverse transcription to obtain isolated selected cDNA species.

Claim 31. (Amended) The gene transcript pattern probe kit as claimed in Claim 29, further comprising, for comparative purposes, a standard gene transcript pattern obtained by a method comprising the steps of:

- (a) isolating mRNA from cells of one or more test eukaryotic organisms which are known to have said disease or condition or a stage thereof (diseased sample), wherein said cells are obtained from, and originate from, a part of said organism distant to the area of said disease, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA; and
- (b) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to the isolated

selected mRNA species or isolated selected cDNA species which are immobilized in the gene transcript pattern probe kit of Claim 29, and assessing the amount of hybridization so as to obtain said standard gene transcript pattern, wherein the isolated selected mRNA species or isolated selected cDNA species are specific for said disease or condition or stage thereof.

Claim 32. (Twice Amended) A method of preparing a gene transcript pattern probe kit comprising the steps of:

- (a) isolating mRNA from cells of one or more eukaryotic organisms which are known to have a disease or condition or a stage thereof (diseased sample), wherein said cells are obtained from, and originate from, a part of said organism distant to the area of said disease, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) isolating mRNA from corresponding cells of one or more corresponding normal eukaryotic organisms (normal sample), wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (c) separating, by a non-sequence based separation technique, mRNA species or cDNA species present within each of the resulting isolated mRNA or isolated cDNA of step (a) and step (b), wherein the resulting

separated mRNA species are optionally subjected to reverse transcription to obtain separated cDNA species;

- (d) selecting two or more mRNA species or two or more cDNA species from the resulting separated mRNA species or resulting separated cDNA species obtained in step (c), respectively, which are present at a different level in the normal sample than in the diseased sample by identifying a signal corresponding to each mRNA species or cDNA species, wherein the resulting selected two or more mRNA species are optionally subjected to reverse transcription to obtain two or more selected cDNA species;
- (e) isolating the resulting two or more selected mRNA species or resulting two or more selected cDNA species obtained in step (d) to obtain isolated selected mRNA species or isolated selected cDNA species, wherein the resulting isolated selected mRNA species are optionally subjected to reverse transcription to obtain isolated selected cDNA species; and
- (f) immobilizing the resulting isolated selected mRNA species or isolated selected cDNA species of step (e) on at least one solid support so as to form a gene transcript pattern probe kit.

Claim 33. (Twice Amended) A method of preparing a standard gene transcript pattern characteristic of a

disease or condition or stage thereof of a eukaryotic organism comprising the steps of:

- (a) isolating mRNA from cells of one or more test eukaryotic organisms known to have said disease or condition or stage thereof, wherein said cells are obtained from, and originate from, a part of said organism distant to the area of said disease, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA; and
- (b) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to the isolated selected mRNA species or isolated selected cDNA species which are immobilized in the gene transcript pattern probe kit of Claim 29, and assessing the amount of hybridization so as to obtain said standard gene transcript pattern, wherein the isolated selected mRNA species or isolated selected cDNA species are specific for said disease or condition or stage thereof.

Claim 34. (Twice Amended) A method of preparing a test gene transcript pattern comprising the steps of:

- (a) isolating mRNA from cells of a test eukaryotic organism, wherein said cells are obtained from, and originate from, a part of said organism distant to the area of said disease, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA; and

- (b) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to the isolated selected mRNA species or isolated selected cDNA species which are immobilized in the gene transcript pattern probe kit of Claim 29, and assessing the amount of hybridization so as to obtain said test gene transcript pattern, wherein the isolated selected mRNA species or isolated selected cDNA species are specific for a desired disease or condition or stage thereof.

Claim 35. (Twice Amended) A method of diagnosing or identifying a disease or condition or stage thereof in a test eukaryotic organism comprising the steps of:

- (a) isolating mRNA from cells of a test eukaryotic organism, wherein said cells are obtained from, and originate from, a part of said organism distant to the area of said disease, wherein the resulting isolated mRNA is optionally subjected to reverse transcription to obtain isolated cDNA;
- (b) hybridizing the resulting isolated mRNA or isolated cDNA of step (a) to the isolated selected mRNA species or isolated selected cDNA species which are immobilized in the gene transcript pattern probe kit of Claim 29, and assessing the amount of hybridization so as to obtain a hybridization pattern, wherein the isolated selected mRNA species or isolated selected

- cDNA species are specific for said disease or condition or stage thereof; and
- (c) comparing the resulting hybridization pattern obtained in step (b) with a hybridization pattern obtained by hybridizing isolated mRNA or isolated cDNA prepared from corresponding cells from one or more corresponding eukaryotic organisms known to have said disease or condition or stage thereof to the isolated selected mRNA species or isolated selected cDNA species which are immobilized in said gene transcript pattern probe kit and assessing the amount of hybridization, so as to determine the degree of correlation indicative of the presence of said disease or condition or stage thereof, and so as to diagnose or identify said disease or condition or a stage thereof in said test eukaryotic organism.

Please add the following new claim:

- Claim 36. The method as claimed in Claim 18, wherein said disease is selected from the group consisting of stomach cancer, lung cancer, breast cancer, prostate gland cancer, bowel cancer and skin cancer. --